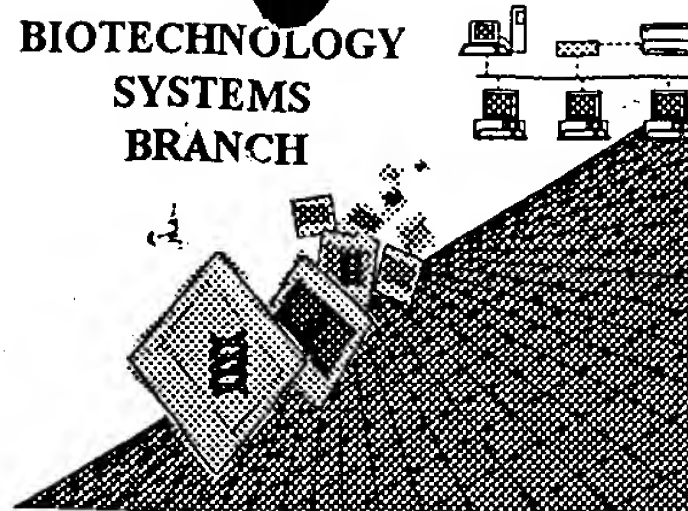


RAW SEQUENCE LISTING ERROR REPORT



0590
0831

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/844,157
Source: O/P
Date Processed by STIC: 10/11/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/841,157

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) 1-44 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/841,157

DATE: 10/11/2001
 TIME: 10:40:08

Input Set : A:\US09841157SEQLIST.txt
 Output Set: N:\CRF3\10112001\I841157.raw

3 <110> APPLICANT: Taitec Co., Ltd.
 W--> 4 <120> TITLE OF INVENTION: Method for identifying an organism by its genotype
 C--> 5 <140> CURRENT APPLICATION NUMBER: US/09/841,157
 C--> 5 <141> CURRENT FILING DATE: 2001-04-25
 E--> 5 <160> NUMBER OF SEQ ID:
 W--> 0 <130> FILE REFERENCE:
 E--> 5 <160> NUMBER OF SEQ ID NOS:

ERRORED SEQUENCES

W--> 6 <210> SEQ ID NO: 1
 7 <211> LENGTH: 204
 8 <212> TYPE: DNA
 W--> 9 <211> LENGTH: unknown
 W--> 10 <213> ORGANISM:
 E--> 10 <400> SEQUENCE: 0
 11 tgctacgtct ctccgatgc tgtctttcgc tgctgagggt gacgatcccg caaaagcggc 60
 12 ctttgactcc ctgcaagcct cagcgaccga atatatcggt tatgcgtggg cgatggttgt 120
 13 tgtcattgtc ggcgcaacta tcggtatcaa gctgtttaag aaattcacct cgaaagcaag 180
 14 ctgataaacc gatagaattc aagg 204
 55 <210> SEQ ID NO: 8
 E--> 56 <211>12
 57 <212> TYPE: DNA
 58 <211> LENGTH: unknown
 W--> 59 <213> ORGANISM:
 W--> 59 <400> SEQUENCE: 8
 E--> 60 aaatttaaat tt 12
 61 <210> SEQ ID NO: 9
 62 <211> LENGTH: 12
 63 <212> TYPE: DNA
 W--> 64 <211> LENGTH: unknown
 W--> 65 <213> ORGANISM:
 W--> 65 <400> SEQUENCE: 9
 E--> 66 aattaattaa tt
 187 <210> SEQ ID NO: 30
 188 <211> LENGTH: 12
 189 <212> TYPE: DNA
 W--> 190 <211> LENGTH: unknown
 W--> 191 <213> ORGANISM:
 W--> 191 <400> SEQUENCE: 30
 E--> 192 gatcacctcc tta 13)
 193 <210> SEQ ID NO: 31
 194 <211> LENGTH: 12
 195 <212> TYPE: DNA
 W--> 196 <211> LENGTH: unknown
 W--> 197 <213> ORGANISM:

Does Not Comply
 Corrected Diskette Needed

see following pages

many errors

*Please consult
 Sequence Rules*

09/84/157

2

~~SEQUENCE LISTING~~

<110> Taitec Co., Ltd.

<120> Method for identifying an organism by its genotype

<160> ~~mandatory response needed (44 shown)~~ → <1407> <1417>

<210>1

<211>204

<212>DNA

<213> ~~<211>unknown~~ see item 11 on Ena summary sheet

<400>1

tgctacgtct cttccgatgc tgtcttttcgc tgctgagggg gacgatcccg caaaagcggc 60
 ctttgactcc ctgcaagcct cagcgaccga atatatcggt tatgcgtggg cgatgggttg 120
 tgtcattgtc ggcgcaacta tcggtatcaa gctgtttaag aaattcacct cgaaagcaag 180
 ctgataaacc gatagaattc aagg 204

<210>2

<211>286

<212>DNA

<211>unknown

<400>2

attggcgcgc tggcaacgat tgcccgtgcg caaggcggcg taatgcgtca tgtcaaaccg 60
 cacggcatgt tgtacaacca ggcggcgaaa gaagcacaac tggcagacgc catcgccaga 120
 gcggtatacg cttgcgatcc agcattgatt ctgcgcgggc tggcggggaag cgagctgatt 180
 cgtgcaggca agcaatatgg tctgacaacg cgcgaggaag tgtttgccga tcgcggttat 240
 caggctgacg gctcgtcgtg gccgcgaagc cagtcaggcg cgttga 286

<210>3

<211>12

<212>DNA

<211>unknown

<400>3

cagtcaggac gt 12

<210>4

<211>12

<212>DNA

<211>unknown

<400>4

agaacgcgcc tg 12

<210>5

<211>12

<212>DNA

<211>unknown

<400>5

cgtcgctatt aa 12

<210>6

<211>12

<212>DNA

<211>unknown

<400>6

cagggcgcgt ac 12

<210>7

<211>12

<212>DNA

<211>unknown

<400>7

aaaaaaaaaa ad 12

<210>8

<211>12

<212>DNA

insert these
mandatorynumeric
identifiers
and responses

Please ensure
all <211> responses
= match actual
number of bases

global
error

<211>unknown
 <400>8
 aaattttaaat tt 12
 <210>9
 <211>12
 <212>DNA
 <211>unknown
 <400>9
 aattaattaa tt
 <210>10
 <211>12
 <212>DNA
 <211>unknown
 <400>10
 acgacgacga cg 12
 <210>11
 <211>12
 <212>DNA
 <211>unknown
 <400>11
 atatatatat at 12
 <210>12
 <211>12
 <212>DNA
 <211>unknown
 <400>12
 cccccccccc cc 12
 <210>13
 <211>12
 <212>DNA
 <211>unknown
 <400>13
 ccggccggcc gg 12
 <210>14
 <211>12
 <212>DNA
 <211>unknown
 <400>14
 ctctctctct ct 12
 <210>15
 <211>12
 <212>DNA
 <211>unknown
 <400>15
 gggggggggg gg 12
 <210>16
 <211>12
 <212>DNA
 <211>unknown
 <400>16
 gagagagaga ga 12
 <210>17
 <211>12
 <212>DNA
 <211>unknown
 <400>17
 ggccggccgg cc 12

12 ← insert

<210>18
<211>12
<212>DNA
<211>unknown
<400>18
tttttttttt tt 12
<210>19
<211>12
<212>DNA
<211>unknown
<400>19
tttgggtttg gg 12
<210>20
<211>12
<212>DNA
<211>unknown
<400>20
tgctgctgct gc 12
<210>21
<211>12
<212>DNA
<211>unknown
<400>21
tatatatacc ac 12
<210>22
<211>12
<212>DNA
<211>unknown
<400>22
gggcggcgac ct 12
<210>23
<211>12
<212>DNA
<211>unknown
<400>23
aggtcgccgc cc 12
<210>24
<211>12
<212>DNA
<211>unknown
<400>24
ggggtcgagg gg 12
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<211>12
<212>DNA
<211>unknown
<400>25
gctaaaadaa aa 12
<210>26
<211>12
<212>DNA
<211>unknown
<400>26
caattctaca ac 12
<210>27
<211>12
<212>DNA

09/841,157 \$

<211>unknown

<400>27

acgagcgagc gc 12

<210>28

<211>12

<212>DNA

<211>unknown

<400>28

tataattata at 12

<210>29

<211>12

<212>DNA

<211>unknown

<400>29

attataatta ta 12

<210>30

<211>12

<212>DNA

<211>unknown

<400>30

gatcacctcc tta 13 *delete parenthesis*

<210>31

<211>12/13

<212>DNA

<211>unknown

<400>31

taaggaggtg atc 13

<210>32

<211>12

<212>DNA

<211>unknown

<400>32

cccacccacc ca 12

<210>33

<211>12

<212>DNA

<211>unknown

<400>33

tgggtgggtg gg 12

<210>34

<211>25

<212>DNA

<211>unknown

<400>34

gaggaaacag ctatgagatc ttctc 25

<210>35

<211>25

<212>DNA

<211>unknown

<400>35

caggaaacag ctatgacgtt ctcac 25

<210>36

<211>16

<212>DNA

<211>unknown

<400>36

ggcgatatcc ctgaaa 16

<210>37
 <211>16
 <212>DNA
 <211>unknown
 <400>37

tattatttcc gcaaag 16
 <210>38
 <211>17
 <212>DNA
 <211>unknown
 <400>38

caggaaacag ctatgac 17
 <210>39
 <211>12

<212>DNA
 <211>unknown
 <400>39

delete

cy3-agaacgcgcc tg 12
 <210>40
 <211>18/17

show bases only - no dashes or extraneous material

<212>DNA
 <211>unknown
 <400>40

FITC-caggaaaca gctatgac 18/17
 <210>41
 <211>31

<212>DNA
 <211>unknown
 <400>41

delete

FITC-tgctacgtct cttccgatgc tgtctttcgc t 31
 <210>42
 <211>31
 <212>DNA
 <211>unknown
 <400>42

delete space

delete

cy3-tgctacgtct cttccgatgc tgtctttcgc t 31
 <210>43
 <211>12
 <212>DNA
 <211>unknown
 <400>43

delete

HEX-gaacctcccg ac 12
 <210>44
 <211>12
 <212>DNA
 <211>unknown
 <400>44

delete

TAM-Tgctgctgct gc 12

use lower-case letters

First

Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.